



IFWO

RAW SEQUENCE LISTING

DATE: 08/02/2004

PATENT APPLICATION: US/10/724,301

TIME: 15:07:13

Input Set : A:\1-1411 SEQUENCE LISTING.txt

Output Set: N:\CRF4\08022004\J724301.raw

3 <110> APPLICANT: Enenkel, Barbara
 4 Fieder, Juergen
 5 Otto, Ralf
 6 Sautter, Kerstin
 7 Bergemann, Klaus
 9 <120> TITLE OF INVENTION: Neomycin-Phosphotransferase Genes and Methods
 10 for the Selection of Recombinant Cells Producing
 11 High Levels of a Desired Gene Product
 13 <130> FILE REFERENCE: 1/1411
 C--> 15 <140> CURRENT APPLICATION NUMBER: US/10/724,301
 16 <141> CURRENT FILING DATE: 2003-11-26
 18 <150> PRIOR APPLICATION NUMBER: US 60/431,535
 19 <151> PRIOR FILING DATE: 2002-12-06
 21 <150> PRIOR APPLICATION NUMBER: US 60/487,902
 22 <151> PRIOR FILING DATE: 2003-07-17
 24 <150> PRIOR APPLICATION NUMBER: DE 102 56 081
 25 <151> PRIOR FILING DATE: 2002-11-29
 27 <150> PRIOR APPLICATION NUMBER: DE 103 30 686
 28 <151> PRIOR FILING DATE: 2003-07-08
 30 <160> NUMBER OF SEQ ID NOS: 55
 32 <170> SOFTWARE: PatentIn Ver. 3.1
 34 <210> SEQ ID NO: 1
 35 <211> LENGTH: 795
 36 <212> TYPE: DNA
 37 <213> ORGANISM: Escherichia coli
 39 <400> SEQUENCE: 1
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 41 ggctatgact gggcacaaca gacaatcggc tgctctgatg ccgccgtgtt ccggetgtca 120
 42 gcgcaggggc gcccggttct ttttgtcaag accgacctgt ccggtgccct gaatgaactg 180
 43 caagacgagg cagcgcggct atcgtggctg gccacgacgg gcgttccttg cgcagctgtg 240
 44 ctcgacgttg tcaactgaagc gggaaggac tggctgctat tgggcgaagt gccggggcag 300
 45 gatctcctgt catctcacct tgctcctgcc gagaaagtat ccatcatggc tgatgcaatg 360
 46 cggcggctgc atacgcttga tccggctacc tgcccattcg accaccaagc gaaacatcgc 420
 47 atcgagcgag cagtgactcg gatggaagcc ggtcttgctg atcaggatga tctggacgaa 480
 48 gagcatcagg ggctcgcgcc agccgaactg ttcgccaggc tcaaggcgag catgcccagc 540
 49 ggcgaggatc tcgtcgtgac ccatggcgat gcctgcttgc cgaatatcat ggtggaaaat 600
 50 ggccgctttt ctggattcat cgactgtggc cggttgggtg tggcggaccg ctatcaggac 660
 51 atagcgttgg ctaccctgta tattgctgaa gagcttggcg gcgaatgggc tgaccgcttc 720
 52 ctcggtgcttt acggtatcgc cgctcccgat tcgcagcgca tcgccttcta tcgccttctt 780
 53 gacgagttct tctga
 56 <210> SEQ ID NO: 2
 57 <211> LENGTH: 264
 58 <212> TYPE: PRT



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59 <213> ORGANISM: Escherichia coli

61 <400> SEQUENCE: 2

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62 Met Ile Glu Gln Asp Gly Leu His Ala Gly Ser Pro Ala Ala Trp Val
63   1           5           10           15
65 Glu Arg Leu Phe Gly Tyr Asp Trp Ala Gln Gln Thr Ile Gly Cys Ser
66           20           25           30
68 Asp Ala Ala Val Phe Arg Leu Ser Ala Gln Gly Arg Pro Val Leu Phe
69           35           40           45
71 Val Lys Thr Asp Leu Ser Gly Ala Leu Asn Glu Leu Gln Asp Glu Ala
72           50           55           60
74 Ala Arg Leu Ser Trp Leu Ala Thr Thr Gly Val Pro Cys Ala Ala Val
75   65           70           75           80
77 Leu Asp Val Val Thr Glu Ala Gly Arg Asp Trp Leu Leu Leu Gly Glu
78           85           90           95
80 Val Pro Gly Gln Asp Leu Leu Ser Ser His Leu Ala Pro Ala Glu Lys
81           100          105          110
83 Val Ser Ile Met Ala Asp Ala Met Arg Arg Leu His Thr Leu Asp Pro
84           115          120          125
86 Ala Thr Cys Pro Phe Asp His Gln Ala Lys His Arg Ile Glu Arg Ala
87           130          135          140
89 Arg Thr Arg Met Glu Ala Gly Leu Val Asp Gln Asp Asp Leu Asp Glu
90   145          150          155          160
92 Glu His Gln Gly Leu Ala Pro Ala Glu Leu Phe Ala Arg Leu Lys Ala
93           165          170          175
95 Ser Met Pro Asp Gly Glu Asp Leu Val Val Thr His Gly Asp Ala Cys
96           180          185          190
98 Leu Pro Asn Ile Met Val Glu Asn Gly Arg Phe Ser Gly Phe Ile Asp
99           195          200          205
101 Cys Gly Arg Leu Gly Val Ala Asp Arg Tyr Gln Asp Ile Ala Leu Ala
102           210          215          220
104 Thr Arg Asp Ile Ala Glu Leu Gly Gly Glu Trp Ala Asp Arg Phe
105   225          230          235          240
107 Leu Val Leu Tyr Gly Ile Ala Ala Pro Asp Ser Gln Arg Ile Ala Phe
108           245          250          255
110 Tyr Arg Leu Leu Asp Glu Phe Phe
111           260

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114 <210> SEQ ID NO: 3

115 <211> LENGTH: 795

116 <212> TYPE: DNA

117 <213> ORGANISM: Artificial sequence

119 <220> FEATURE:

120 <223> OTHER INFORMATION: Neomycin mutant E182G

122 <400> SEQUENCE: 3

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124 ggctatgact gggcacaaca gacaatcggc tgctctgatg ccgccgtggt ccggctgtca 120
125 gcgcaggggc gcccggttct ttttgtcaag accgacctgt ccggtgccct gaatgaactg 180
126 caagacgagg cagcgcgggt atcgtggctg gccacgacgg gcgttccttg cgcagctgtg 240
127 ctgcacgttg tcactgaagc gggaaggac tggtgctat tgggcgaagt gccggggcag 300
128 gatctcctgt catctcacct tgctcctgcc gagaaagtat ccatcatggc tgatgcaatg 360

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129 cggcggtctgc atacgcttga tccggctacc tgcccattcg accaccaagc gaaacatcgc 420
130 atcgagcgag cacgtactcg gatggaagcc ggtcttgcg atcaggatga tctggacgaa 480
131 gagcatcagg ggctcgcgcc agccgaactg ttccgccaggc tcaaggcgag catgcccgcac 540
132 ggccggggatc tcgtcgtgac ccatggcgat gcctgcttgc cgaatatcat ggtggaaaat 600
133 ggccgctttt ctggattcat cgactgtggc cggctgggtg tggcggaccg ctatcaggac 660
134 atagcgttgg ctaccctgta tattgctgaa gagcttggcg gcgaatgggc tgaccgcttc 720
135 ctctgtcttt acggtatcgc cgctcccgat tcgcagcgca tcgccttcta tcgccttctt 780
136 gacgagttct tctga 795

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139 <210> SEQ ID NO: 4

140 <211> LENGTH: 264

141 <212> TYPE: PRT

142 <213> ORGANISM: Artificial sequence

144 <220> FEATURE:

145 <223> OTHER INFORMATION: Neomycin mutant E182G

147 <400> SEQUENCE: 4

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148 Met Ile Glu Gln Asp Gly Leu His Ala Gly Ser Pro Ala Ala Trp Val
149   1           5           10           15
151 Glu Arg Leu Phe Gly Tyr Asp Trp Ala Gln Gln Thr Ile Gly Cys Ser
152           20           25           30
154 Asp Ala Ala Val Phe Arg Leu Ser Ala Gln Gly Arg Pro Val Leu Phe
155           35           40           45
157 Val Lys Thr Asp Leu Ser Gly Ala Leu Asn Glu Leu Gln Asp Glu Ala
158           50           55           60
160 Ala Arg Leu Ser Trp Leu Ala Thr Thr Gly Val Pro Cys Ala Ala Val
161   65           70           75           80
163 Leu Asp Val Val Thr Glu Ala Gly Arg Asp Trp Leu Leu Leu Gly Glu
164           85           90           95
166 Val Pro Gly Gln Asp Leu Leu Ser Ser His Leu Ala Pro Ala Glu Lys
167           100          105          110
169 Val Ser Ile Met Ala Asp Ala Met Arg Arg Leu His Thr Leu Asp Pro
170           115          120          125
172 Ala Thr Cys Pro Phe Asp His Gln Ala Lys His Arg Ile Glu Arg Ala
173           130          135          140
175 Arg Thr Arg Met Glu Ala Gly Leu Val Asp Gln Asp Asp Leu Asp Glu
176   145          150          155          160
178 Glu His Gln Gly Leu Ala Pro Ala Glu Leu Phe Ala Arg Leu Lys Ala
179           165          170          175
181 Ser Met Pro Asp Gly Gly Asp Leu Val Val Thr His Gly Asp Ala Cys
182           180          185          190
184 Leu Pro Asn Ile Met Val Glu Asn Gly Arg Phe Ser Gly Phe Ile Asp
185           195          200          205
187 Cys Gly Arg Leu Gly Val Ala Asp Arg Tyr Gln Asp Ile Ala Leu Ala
188           210          215          220
190 Thr Arg Asp Ile Ala Glu Leu Gly Gly Glu Trp Ala Asp Arg Phe
191   225          230          235          240
193 Leu Val Leu Tyr Gly Ile Ala Ala Pro Asp Ser Gln Arg Ile Ala Phe
194           245          250          255
196 Tyr Arg Leu Leu Asp Glu Phe Phe
197           260

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200 <210> SEQ ID NO: 5
201 <211> LENGTH: 795
202 <212> TYPE: DNA
203 <213> ORGANISM: Artificial sequence
205 <220> FEATURE:
206 <223> OTHER INFORMATION: Neomycin mutant W91A
208 <400> SEQUENCE: 5
209 atgattgaac aagatggatt gcacgcaggt tctccggccg cttgggtgga gaggctattc 60
210 ggctatgact gggcacaaca gacaatcggc tgctctgatg ccgccgtggt ccggctgtca 120
211 gcgcaggggc gcccggttct ttttgtcaag accgacctgt ccggtgccct gaatgaactg 180
212 caagacgagg cagcgcggct atcgtggctg gccacgacgg gcgttccttg cgcagctgtg 240
213 ctgcagcttg tcaactgaagc gggaaaggac gcgtgctat tgggcgaagt gccggggcag 300
214 gatctcctgt catctcacct tgctcctgcc gagaaagtat ccatacatggc tgatgcaatg 360
215 cggcggctgc atacgcttga tccggctacc tgcccattcg accaccaagc gaaacatcgc 420
216 atcgagcgag cagctactcg gatggaagcc ggtcttgctg atcaggatga tctggacgaa 480
217 gagcatcagg ggctcgcgcc agccgaactg ttcgccaggc tcaaggcgag catgcccgcac 540
218 ggcgaggatc tcgtcgtgac ccattggcgat gcctgcttgc cgaatatcat ggtggaaaat 600
219 ggccgctttt ctggattcat cgactgtggc cggtggttg tggcggaccg ctatcaggac 660
220 atagcgttgg ctacccgtga tattgctgaa gagcttggcg gcgaatgggc tgaccgcttc 720
221 ctgctgcttt acggtatcgc cgtcccgat tcgcagcgca tcgcttcta tcgcttctt 780
222 gacgagttct tctga 795
225 <210> SEQ ID NO: 6
226 <211> LENGTH: 264
227 <212> TYPE: PRT
228 <213> ORGANISM: Artificial sequence
230 <220> FEATURE:
231 <223> OTHER INFORMATION: Neomycin mutant W91A
233 <400> SEQUENCE: 6
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235 1 5 10 15
237 Glu Arg Leu Phe Gly Tyr Asp Trp Ala Gln Gln Thr Ile Gly Cys Ser
238 20 25 30
240 Asp Ala Ala Val Phe Arg Leu Ser Ala Gln Gly Arg Pro Val Leu Phe
241 35 40 45
243 Val Lys Thr Asp Leu Ser Gly Ala Leu Asn Glu Leu Gln Asp Glu Ala
244 50 55 60
246 Ala Arg Leu Ser Trp Leu Ala Thr Thr Gly Val Pro Cys Ala Ala Val
247 65 70 75 80
249 Leu Asp Val Val Thr Glu Ala Gly Arg Asp Ala Leu Leu Leu Gly Glu
250 85 90 95
252 Val Pro Gly Gln Asp Leu Leu Ser Ser His Leu Ala Pro Ala Glu Lys
253 100 105 110
255 Val Ser Ile Met Ala Asp Ala Met Arg Arg Leu His Thr Leu Asp Pro
256 115 120 125
258 Ala Thr Cys Pro Phe Asp His Gln Ala Lys His Arg Ile Glu Arg Ala
259 130 135 140
261 Arg Thr Arg Met Glu Ala Gly Leu Val Asp Gln Asp Asp Leu Asp Glu
262 145 150 155 160
264 Glu His Gln Gly Leu Ala Pro Ala Glu Leu Phe Ala Arg Leu Lys Ala

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265          165          170          175
267 Ser Met Pro Asp Gly Glu Asp Leu Val Val Thr His Gly Asp Ala Cys
268          180          185          190
270 Leu Pro Asn Ile Met Val Glu Asn Gly Arg Phe Ser Gly Phe Ile Asp
271          195          200          205
273 Cys Gly Arg Leu Gly Val Ala Asp Arg Tyr Gln Asp Ile Ala Leu Ala
274          210          215          220
276 Thr Arg Asp Ile Ala Glu Glu Leu Gly Gly Glu Trp Ala Asp Arg Phe
277 225          230          235          240
279 Leu Val Leu Tyr Gly Ile Ala Ala Pro Asp Ser Gln Arg Ile Ala Phe
280          245          250          255
282 Tyr Arg Leu Leu Asp Glu Phe Phe
283          260
286 <210> SEQ ID NO: 7
287 <211> LENGTH: 795
288 <212> TYPE: DNA
289 <213> ORGANISM: Artificial sequence
291 <220> FEATURE:
292 <223> OTHER INFORMATION: Neomycin mutant V198G
294 <400> SEQUENCE: 7
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296 ggctatgact gggcacaaca gacaatcggc tgctctgatg ccgccgtgtt cggctgtca 120
297 gcgcaggggc gcccggttct ttttgtcaag accgacctgt ccggtgccct gaatgaactg 180
298 caagacgagg cagcgcggct atcgtggctg gccacgacgg gcgttccttg cgcagctgtg 240
299 ctgcacgttg tcaactgaagc gggaaggac tggctgctat tgggcgaagt gccggggcag 300
300 gatctcctgt catctcacct tgctcctgcc gagaaagtat ccatcatggc tgatgcaatg 360
301 cggcggtgcg atacgcttga tccggctacc tgccattcgc accaccaagc gaaacatcgc 420
302 atcgagcgag cacgtactcg gatggaagcc ggtcttgctg atcaggatga tctggacgaa 480
303 gagcatcagg ggctcgcgcc agccgaactg ttcgccaggc tcaaggcgag catgcccgcac 540
304 ggcgaggatc tcgtcgtgac ccatggcgat gctgcttgcc cgaatatcat gggggaaaat 600
305 ggccgctttt ctggattcat cgactgtggc cggctgggtg tggcggaccg ctatcaggac 660
306 atagcgttgg ctaccctgga tattgctgaa gagcttggcg gcgaatgggc tgaccgcttc 720
307 ctgctgcttt acggtatcgc cgctcccgat tcgcagcgca tcgccttcta tcgccttctt 780
308 gacgagttct tctga 795
311 <210> SEQ ID NO: 8
312 <211> LENGTH: 264
313 <212> TYPE: PRT
314 <213> ORGANISM: Artificial sequence
316 <220> FEATURE:
317 <223> OTHER INFORMATION: Neomycin mutant V198G
319 <400> SEQUENCE: 8
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323 Glu Arg Leu Phe Gly Tyr Asp Trp Ala Gln Gln Thr Ile Gly Cys Ser
324 20 25 30
326 Asp Ala Ala Val Phe Arg Leu Ser Ala Gln Gly Arg Pro Val Leu Phe
327 35 40 45
329 Val Lys Thr Asp Leu Ser Gly Ala Leu Asn Glu Leu Gln Asp Glu Ala
330 50 55 60

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VERIFICATION SUMMARY

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Input Set : A:\1-1411 SEQUENCE LISTING.txt

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L:15 M:270 C: Current Application Number differs, Replaced Current Application Number